SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
      Shah, Purvi
      Corley, Neil C.

(ii) TITLE OF THE INVENTION: HUMAN MEMBRANE RECYCLING
   PROTEINS

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Dr.
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: To Be Assigned
 (B) FILING DATE: Filed Herewith
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 09/360,125
 (B) FILING DATE: July 23, 1999

(vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: 09/004,502
 (B) FILING DATE: January 8, 1998

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Billings, Lucy J.
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0456 US

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 650-855-0555
 (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: TONGTUT01
 (B) CLONE: 980615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
1               5                   10                  15
Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
```

```
             20                          25                          30
Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
         35                          40                          45
Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
     50                          55                          60
Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
65                          70                          75                          80
Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
                 85                          90                          95
Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
                 100                         105                         110
Leu Asp Arg Arg Glu Arg Glu Leu Gln His Ala Ala Leu Gly Gly Thr
         115                         120                         125
Ala Thr Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Phe Cys Pro Val
     130                         135                         140
Gln Pro Cys Phe Phe Gln Asp Ile Ser Met Glu Ile Pro Gln Glu Phe
145                         150                         155                         160
Gln Lys Thr Val Ser Thr Met Tyr Tyr Leu Trp Met Cys Ser Thr Leu
                 165                         170                         175
Ala Leu Leu Leu Asn Phe Leu Ala Cys Leu Ala Ser Phe Cys Val Glu
                 180                         185                         190
Thr Asn Asn Gly Ala Gly Phe Gly Leu Ser Ile Leu Trp Val Leu Leu
         195                         200                         205
Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Met Tyr Lys Ala
     210                         215                         220
Phe Arg Ser Asp Ser Ser Phe Asn Phe Phe Val Phe Phe Phe Ile Phe
225                         230                         235                         240
Phe Val Gln Asp Val Leu Phe Val Leu Gln Ala Ile Gly Ile Pro Gly
                 245                         250                         255
Trp Gly Phe Ser Gly Trp Ile Ser Ala Leu Val Val Pro Lys Gly Asn
                 260                         265                         270
Thr Ala Val Ser Val Leu Met Leu Leu Val Ala Leu Leu Phe Thr Gly
         275                         280                         285
Ile Ala Val Leu Gly Ile Val Met Leu Lys Arg Ile His Ser Leu Tyr
     290                         295                         300
Arg Arg Thr Gly Ala Ser Phe Gln Lys Ala Gln Gln Glu Phe Ala Ala
305                         310                         315                         320
Gly Val Phe Ser Asn Pro Ala Val Arg Thr Ala Ala Ala Asn Ala Ala
                 325                         330                         335
Ala Gly Ala Ala Glu Asn Ala Phe Arg Ala Pro
         340                         345
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1521 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
        (A) LIBRARY: TONGTUT01
        (B) CLONE: 980615

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
NGACGCAGGC GCAACCCACG GCTGCTGCGG GGATCCTTGT GGCCCTTCCG GTCGATGGAA      60
CCAATCCGTG CACAGAGAAG CGGGGCGAAC TGAGGCGAGT GAAGTGGACT CTGAGGGCTA     120
CCGCTACCGC CACTGCTGCG GCAGGGGCGT GGAGGGCAGA GGGCCGCGGA GGCCGCAGTT     180
GCAAACATGG CTCAGAGCAG AGACGGCGGA AACCCGTTCG CCGAGCCCAG CGAGCTTGAC     240
AACCCCTTTC AGGACCCAGC TGTGATCCAG CACCGACCCA GCCGGCAGTA TGCCACGCTT     300
GACGTCTACA ACCCTTTTGA GACCCGGGAG CCACCACCAG CCTATGAGCC TCCAGCCCCT     360
GCCCCATTGC CTCCACCCTC AGCTCCCTCC TTGCAGCCCT CGAGAAAGCT CAGCCCCACA     420
GAACCTAAGA ACTATGGCTC ATACAGCACT CAGGCCTCAG CTGCAGCAGC CACAGCTGAG     480
CTGCTGAAGA AACAGGAGGA GCTCAACCGG AAGGCAGAGG AGTTGGACCG AAGGGAGCGA     540
GAGCTGCAGC ATGCTGCCCT GGGGGGCACA GCTACTCGAC AGAACAATTG GCCCCCTCTA     600
CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT TTCCAGGACA TCTCCATGGA GATCCCCCAA     660
```

```
GAATTTCAGA AGACTGTATC CACCATGTAC TACCTCTGGA TGTGCAGCAC GCTGGCTCTT    720
CTCCTGAACT TCCTCGCCTG CCTGGCCAGC TTCTGTGTGG AAACCAACAA TGGCGCAGGC    780
TTTGGGCTTT CTATCCTCTG GGTCCTCCTT TTCACTCCCT GCTCCTTTGT CTGCTGGTAC    840
CGCCCCATGT ATAAGGCTTT CCGGAGTGAC AGTTCATTCA ATTTCTTCGT TTTCTTCTTC    900
ATTTTCTTCG TCCAGGATGT GCTCTTTGTC CTCCAGGCCA TTGGTATCCC AGGTTGGGGA    960
TTCAGTGGCT GGATCTCTGC TCTGGTGGTG CCGAAGGGCA ACACAGCAGT ATCCGTGCTC   1020
ATGCTGCTGG TCGCCCTGCT CTTCACTGGC ATTGCTGTGC TAGGAATTGT CATGCTGAAA   1080
CGGATCCACT CCTTATACCG CCGCACAGGT GCCAGCTTTC AGAAGGCCCA GCAAGAATTT   1140
GCTGCTGGTG TCTTCTCCAA CCCTGCGGTG CGAACCGCAG CTGCCAATGC AGCCGCTGGG   1200
GCTGCTGAAA ATGCCTTCCG GGCCCCGTGA CCCCTGACTG GGATGCCCTG GCCCTGCTAC   1260
TTGAGGGAGC TGACTTAGCT CCCGTCCCTA AGGTCTCTGG GACTTGGAGA GACATCACTA   1320
ACTGATGGCT CCTCCGTAGT GCTCCCAATC CTATGGCCAT GACTGCTGAA CCTGACAGGC   1380
GTGTGGGGAG TTCACTGTGA CCTAGTCCCC CCATCAGGCC ACACTGCTGC CACCTCTCAC   1440
ACGCCCCAAC CCAGCTTCCC TCTGCTGTGC CACGGCTGTT GCTTCGGTTA TTTAAATAAA   1500
AAGAAAGTGG AACTGGAACT G                                            1521
```

(2) INFORMATION FOR SEQ ID NO:3:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 329 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (vii) IMMEDIATE SOURCE:
        (A) LIBRARY: BRSTNOT01
        (B) CLONE: 412453

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Ser Ala Phe Asp Thr Asn Pro Phe Ala Asp Pro Val Asp Val Asn
1               5                   10                  15
Pro Phe Gln Asp Pro Ser Val Thr Gln Leu Thr Asn Ala Pro Gln Gly
            20                  25                  30
Gly Leu Ala Glu Phe Asn Pro Phe Ser Glu Thr Asn Ala Ala Thr Thr
        35                  40                  45
Val Pro Val Thr Gln Leu Pro Gly Ser Ser Gln Pro Ala Val Leu Gln
    50                  55                  60
Pro Ser Val Glu Pro Thr Gln Pro Thr Pro Gln Ala Val Val Ser Ala
65                  70                  75                  80
Ala Gln Ala Gly Leu Leu Arg Gln Gln Glu Glu Leu Asp Arg Lys Ala
                85                  90                  95
Ala Glu Leu Glu Arg Lys Glu Arg Glu Leu Gln Asn Thr Val Ala Asn
            100                 105                 110
Leu His Val Arg Gln Asn Asn Trp Pro Pro Leu Pro Ser Trp Cys Pro
        115                 120                 125
Val Lys Pro Cys Phe Tyr Gln Asp Phe Ser Thr Glu Ile Pro Ala Asp
    130                 135                 140
Tyr Gln Arg Ile Cys Lys Met Leu Tyr Tyr Leu Trp Met Leu His Ser
145                 150                 155                 160
Val Thr Leu Phe Leu Asn Leu Leu Ala Cys Leu Ala Trp Phe Ser Gly
                165                 170                 175
Asn Ser Ser Lys Gly Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
            180                 185                 190
Ile Phe Thr Pro Cys Ala Phe Leu Cys Trp Tyr Arg Pro Ile Tyr Lys
        195                 200                 205
Ala Phe Arg Ser Asp Asn Ser Phe Ser Phe Phe Val Phe Phe Phe Val
    210                 215                 220
Phe Phe Cys Gln Ile Gly Ile Tyr Ile Ile Gln Leu Val Gly Ile Pro
225                 230                 235                 240
Gly Leu Gly Asp Ser Gly Trp Ile Ala Ala Leu Ser Thr Leu Asp Asn
                245                 250                 255
His Ser Leu Ala Ile Ser Val Ile Met Met Val Val Ala Gly Phe Phe
            260                 265                 270
Thr Leu Cys Ala Val Leu Ser Val Phe Leu Leu Gln Arg Val His Ser
        275                 280                 285
Leu Tyr Arg Arg Thr Gly Ala Ser Phe Gln Gln Ala Gln Glu Glu Phe
```

61

```
     290                    295                    300
Ser Gln Gly Ile Phe Ser Ser Arg Thr Phe His Arg Ala Ala Ser Ser
305                    310                    315                    320
Ala Ala Gln Gly Ala Phe Gln Gly Asn
                    325
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2434 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
      (A) LIBRARY: BRSTNOT01
      (B) CLONE: 412453

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
NCCGGAAGTG GAGGGTCTAC ACGAAGCGCC GCTGGGTCTG GGTGCCCGGA GGCAGCAGCG      60
TTCGCGGAGT TCGCCCGCTG GCCCCCGATC ACCATGTCGG CTTTCGACAC CAACCCCTTC     120
GCGGACCCAG TGGATGTAAA CCCCTTCCAG GATCCCTCTG TGACCCAGCT GACCAACGCC     180
CCGCAGGGCG GCCTGGCGGA ATTCAACCCC TTCTCAGAGA CAAATGCAGC GACAACAGTT     240
CCTGTCACCC AACTCCCTGG GTCCTCACAG CCAGCGGTTC TCCAGCCATC AGTGGAACCA     300
ACCCAGCCGA CCCCCCAGGC CGTGGTGTCT GCAGCCCAGG CAGGCCTGCT CCGGCAGCAG     360
GAAGAACTGG ACAGGAAAGC TGCCGAGCTG GAACGCAAGG AGCGGGAGCT GCAGAACACT     420
GTAGCCAACT TGCATGTGAG ACAGAACAAC TGGCCCCCTC TGCCCTCGTG GTGCCCTGTG     480
AAGCCCTGCT TCTATCAGGA TTTCTCCACA GAGATCCCTG CCGACTACCA GCGGATATGC     540
AAGATGCTCT ACTATCTGTG GATGTTGCAT TCAGTGACTC TGTTTCTGAA CCTGCTTGCC     600
TGCCTGGCCT GGTTCTCGGG CAACAGCTCC AAGGGAGTGG ACTTTGGCCT CTCCATCCTG     660
TGGTTTCTGA TCTTCACTCC CTGTGCCTTC CTTTGTTGGT ACCGACCCAT CTATAAGGCC     720
TTTAGGTCCG ACAACTCTTT CAGCTTCTTT GTGTTCTTCT TTGTATTTTT TTGTCAAATA     780
GGGATCTACA TCATCCAGTT GGTTGGCATC CCTGGCCTGG GGACAGCGG TTGGATTGCA     840
GCCCTGTCTA CACTGGATAA TCATTCCCTG GCCATATCAG TCATCATGAT GGTGGTGGCT     900
GGCTTCTTCA CCCTCTGTGC CGTGCTCTCA GTCTTCCTCC TGCACGCGGGT GCACTCCCTC     960
TACCGACGGA CAGGGGCCAG CTTCCAGCAG GCCCAGGAGG AGTTTTCCCA GGGCATCTTC    1020
AGCAGCAGAA CCTTCCACAG AGCTGCTTCA TCTGCTGCCC AAGGAGCCTT CCAGGGGAAT    1080
TAGTCCTCCT CTCTTCTCTC CCCCTCAGCC TTTCTCTCGC CTGCCTTCTG AGCTGCACTT    1140
TCCGTGGGTG CCTTATGTGG TGGTGGTTGT GCCCAGCACA GACCTGGCAG GGTTCTTGCC    1200
GTGGCTCTTC CTCCTCCCTC AGCGACCAGC TCTCCCTGGA ACGGGAGGGA CAGGGAATTT    1260
TTTCCCCCTC TATGTACAAA AAAAAACAAA GCTCTCTTTC CTTCTCTGGT GATGGTTTGG    1320
TAGGATTCTT TTGTCTCTGG AAGCAGTGGG ACTGAAGTTC TCTTCGTCCT GTGCACACAC    1380
AGACACCCCC ACACAGTTGG GATCACAGGC TGACCTGGGC CCATCCCAGC TGGAGCTTTC    1440
TGCCAGGGTC CTGGGCCTTG ACTCCCCCAC CCTGCAGGCC TGGCCTGAAT CTGGCTTCTT    1500
AGACACAGCC CAGTCCTTCC TGCCTGGGCT GGGAATAAGC CTCTCACAGG TTCTGGTGGA    1560
CAGATCTGTT CCCCAGGTCA CTCCAGTGGT CTCCAGGCTT CCAGAGAAGG CTGGTTGCCT    1620
CAAGCTCTTC TCTGCCTCAT AAACGGATCC AGAGAAGGCT GGTTGCCTTA AGCTCTTCCC    1680
TGCCTCGTGT TCCTGAGAAA CGGATTAATA GCCCTTTATC CCCCTGCACC CTCCTGCAGG    1740
GGATGGCACT TTGAGCCCTC TGGAGCCCTC CCCTTGCTGA GCCTTACTCT CTTCAGACTT    1800
TCTGAATGTA CAGTGCCGATT GGTTGGGATT TGGGGACCAA AAGGGACCAA GGACACTGAC    1860
CCCAAGCTGT CCTGCCTAGC GTCCAGCGTC TTCTAGGAGG GTGGGGTCTG CCTGTCCTGG    1920
TGTGGTTGGT TTGGCCCTGT TTGCTGTGAC TACCCCCCCC CCTCCCCGAA CCGAGGGACG    1980
GCTGCCTTTG TCTCTGCCTC AGATGCCACC TGCCCCGCCC ATGCTCCCCA TCAGCAGCAT    2040
CCAGACTTTC AGGAAGGGCA GGACCAGCCA GTCCAGAACC GCATCCCTCA GCAGGGACTG    2100
ATAAGCCATC TCTCGGAGGG CCCCCTAATA CCCAGTGGAG TCTGGTTCAC ACCCTGGGGG    2160
GTGTGTCACT GTGATGGGAC ACGTAGGAGT CCACCCTTAA AACCAGCACC CTGTCCCTCG    2220
AGGCTGCCGA GTGGGTGTGT GGACTGGGGT GCCTTCCCAC AAAACTAGCC TCCGGCTCTG    2280
GGCCCGAGAC AGCCGCAGGC CCCAGCCACT GAATGATACT GGCAGCGGCT GGGGTTTTAT    2340
GAACTCCTTT CTGGTATTTT TTCCCCTCTA TGTACAAATG TATATGTTAC GTCTCAATTT    2400
TTGTGCTTAA GTAAAAATAA AAACATTTTC AGAC                                2434
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 338 amino acids
      (B) TYPE: amino acid

```
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
        (A) LIBRARY: GenBank
        (B) CLONE: 487057

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
```

```
Met Ser Asp Phe Asp Ser Asn Pro Phe Ala Asp Pro Asp Leu Asn Asn
 1           5                   10              15
Pro Phe Lys Asp Pro Ser Val Thr Gln Val Thr Arg Asn Val Pro Pro
            20              25              30
Gly Leu Asp Glu Tyr Asn Pro Phe Ser Asp Ser Arg Thr Pro Pro Pro
        35              40              45
Gly Gly Val Lys Met Pro Asn Val Pro Asn Thr Gln Pro Ala Ile Met
    50              55              60
Lys Pro Thr Glu Glu His Pro Ala Tyr Thr Gln Ile Thr Lys Glu His
65              70              75                      80
Ala Leu Ala Gln Ala Glu Leu Leu Lys Arg Gln Glu Glu Leu Glu Arg
            85              90                      95
Lys Ala Ala Glu Leu Asp Arg Arg Glu Arg Glu Met Gln Asn Leu Ser
            100             105             110
Gln His Gly Arg Lys Asn Asn Trp Pro Pro Leu Pro Ser Asn Phe Pro
            115             120             125
Val Gly Pro Cys Phe Tyr Gln Asp Phe Ser Val Asp Ile Pro Val Glu
    130             135             140
Phe Gln Lys Thr Val Lys Leu Met Tyr Tyr Leu Trp Met Phe His Ala
145             150             155                     160
Val Thr Leu Phe Leu Asn Ile Phe Gly Cys Leu Ala Trp Phe Cys Val
            165             170             175
Asp Ser Ser Arg Ala Val Asp Phe Gly Leu Ser Ile Leu Trp Phe Leu
            180             185             190
Leu Phe Thr Pro Cys Ser Phe Val Cys Trp Tyr Arg Pro Leu Tyr Gly
    195             200             205
Ala Phe Arg Ser Asp Ser Ser Phe Arg Phe Phe Val Phe Phe Phe Val
    210             215             220
Tyr Ile Cys Gln Phe Ala Val His Val Leu Gln Ala Ala Gly Phe His
225             230             235                     240
Asn Trp Gly Asn Cys Gly Trp Ile Ser Ser Leu Thr Gly Leu Asn Lys
            245             250             255
Asn Ile Pro Val Gly Ile Met Met Ile Ile Ile Ala Ala Leu Phe Thr
            260             265             270
Ala Ser Ala Val Ile Ser Leu Val Met Phe Lys Lys Val His Gly Leu
    275             280             285
Tyr Arg Thr Thr Gly Ala Ser Phe Glu Lys Ala Gln Gln Glu Phe Ala
    290             295             300
Thr Gly Val Met Ser Asn Lys Thr Val Gln Thr Ala Ala Ala Asn Ala
305             310             315                     320
Ala Ser Thr Ala Ala Thr Ser Ala Ala Gln Asn Ala Phe Lys Gly Asn
            325             330             335
Gln Met
```